

1 GGAAGGTTTAAAGAAAGCCCGCAAGCGCAGGGAAGGCCTCCGGCAGCGGTGGGGAAAGCGCGCGTGCAGCGCGGGGACAGGCACCTGGGCTGGCTAGGATGCTGGT
-31 M S S

121 CCTGGATAAGTGGCATGACCCCGCATGGCGGGCTCTGGGGCTTCTGCTGGCTGGTGGGGCTTCTGGAGGCGCGCTTTCGCCCTGTCCTCCACCGTCTGCAATGTCAGTGCCTCTCGGA
-28 W I R W H G P A M A R L W G F C W L V G F W R A A F A C P T S C K C S A S R I +1

241 TCTGGTGCAGCGACCCCTTCTCTGGCATCGTGCCATTTCCGAGATTGGAGCCTAACAGTGTAGATCCTGAGAACATCACCGAAATTTTCATCGCAAAACACAGAAAAGTTAGAAATCATCA
13 W C S D P S P G I V A F P R L E P N S V D P E N I T E I F I A N Q K R L E I I N F T T A

361 ACGAAGATGATGTTGAAGCTTATGTGGGACTGAGAAATCTGACAATTTGGATTCTGGATTAAATTTGTGGCTCATAAAGCATTTCTGAAAAACAGCAACCTGCAGCAGCATCAATTTTA
53 E D D V E A Y V G L R N L T I V D S G L K F V A H K A F L K N S N L Q H I N F T T A

481 CCGAAACAAACTGACGAGTTTGTCTAGGAAACATTTCCGTACCTTGACTGTCTGTAAGTATCCCTGGTGGGCAATCCATTTACATGCTCCTGTGACATTTATGTGGATCAAGACTCTCC
93 R N K L T S L S R K H F R H L D L S E L I L V G N P F T C S C D I M W I K T L Q

601 AAGAGGCTAAATCCAGTCCAGACACTCAGGATTTGTAAGTCTGCTGAGTATCCCTGGTGGGCAATATTTCCCTGGCAAACTGCAGATACCCAAATTTGGTGGTTTGGCATCTGCAAAATCTGGCG
133 E A K S S P D T Q D L Y C L N E S S K N I P L A N L Q I P N C G L P S A N L A A

721 CACCTAACCTCACTGTGGAGGAAGAAAGTCTATCACATTTATCCTGTAGTGGCAGGTGATCCGGTTCCCTAATATGTTGGGATGTTGGTAACCTGGTTTCCAAACATATGAATGA
173 P N L T V E E G K S I T L S C S V A G D P V P N M Y W D V G N L V S K H M N E T

841 CAAGCCACACACAGGGCTCCTTAAGGATAACTAAACATTTTCATCCGATGACAGTGGGAGCAGATCTCTTGTGGCGGAAATCTTGTAGGAGAGATCAAGATTTCTGTCAACCTCACTG
213 S H T Q G S L R I T N I S S D D S G K Q I S C V A E N L V G E D Q D S V N L T V

961 TGCATTTTCACCAACTATCACATTTCTCGAATCTCCAACCTCAGACCACCACTGGTGCATTCACATTCGAAAGGCAACCCAAACCCAGCGCTTCAGTGGTTCTATATAACGGGGCAA
253 H F A P T I T F L E S P T S D H H W C I P F T V K G N P K P A L Q W F Y N G A I

1081 TATTGAATGAGTCCAAATACATCTGTACTAAAATACATGTTACAAATCACAGGAGTACCACGGCTGCCCTCCAGCTGGATAATCCCACTCACATGAACAATGGGGACTACACTCTTAATAG
293 L N E S K Y I C T K I H V T N H T E Y H G C L Q L D N P T H M N N G D Y T L I A

1201 CCAAGAATGAGTATCGGAAGGATGAGAAACAGATTTCTGCTCACTTCAATGGGCTGGCTGGAAATTCACGATGGTGCAACCCCAATATTCCTGATGTAATTTATGAAGATTTATGAACACTG
333 K N E Y G K D E K Q I S A H F M G W P G I D D G A N P N Y P D V I Y E D Y G T A

1321 CAGCGAATGACATCGGGGACACCACGAACAGAAATGAATCCCTTCCACAGACGTCACTGATAAAAACCGGTGGGAAACATCTCTCGGTCTATGCTGTGGTGGTATGCTGCTGTG
373 A N D I G D T T N R S N E I P S T D V T D K T G R E H L S V Y A V V V I A S V V

1441 TGGGATTTTGCCTTTTGGTAATGCTGTTTCTTAAGTTGGCAAGACACTCCAAGTTTGGCATGAAAGGCCAGCGCTCCGTTATCAGCAATGATGATGACTCTGCCAGCCCCACTCCCAT
413 G F C L L V M L F L L K L A R H S K F G M K G P A S V I S N D D D S A S P L H H

1561 ACATCTCAATGGAGTAACACTCCATCTTCTTCGGAAGGTGGCCCCAGATGCTGTCTATTATTGGAATGACCAAGATCCCTGTCTATTGAAATCCCCAGTACTTTGGCATCACCACAGCT
453 I S N G S N T P S S S E G G P D A V I I G M T K I P V I E N P Q Y F G I T N S Q

ATG

[illegible]

GA

TC2250" 24T99650

1511 TTTTGTGTTTTCATAAGATCCCACTGGATGGTAGCTGAAATAAAGGAAAAGACAGAGAAAGGGGCTGTGGTGCTTGTGGTTGATGCTGCCCATGTAAGCTGGACTCCTGGGACTGCT
436 F V L F H K I P L D G O
1631 GTTGGCTTATCCCGGGAAGTGCTGCTTATCTGGGGTTTTCTGGTAGATGTGGCGGTGTTTGGAGGCTGTACTATATGAAGCCTGCATATACTGTGAGCTGTGATTGGGGAACACCAATG
1751 CAGAGGTAACCTCTCAGGCAGCTAAGCAGCACCTCAAGAAAAACATGTTAAATTAAATGCTTCTCTTACAGTAGTTCAAATACAAAACCTGAAATGAAATCCCATTTGGATTGTACTTCTCT

FIG. 1C

FIG. 2A

1561 TACTTCGTGAGGACACAACTGCCACAAGCCGGACACCTATGTGCAGCAGCATTAAGAGGAGAGACATCGTGTGAAGCGAGACCTTTGGAAAGGTCTTCCTGGCC
 485 Y F R Q G H N C H K K P D T Y V Q H I K R R D I V L K R E L G E G A F G K V F L A
 1681 GAGTGTACAACCTCAGCCCGACCAAGGACAAGATGCTGTGGCTGTGAAGCCCTGAAGGATCCACCCCTGGCTGCCCGAAGGATTTCCAGAGGGAGCGGAGCTGCTCACCACCTG
 525 E C Y N L S P T K D K M L V A V K A L K D P T L A A R K D F Q R E A E L L T N L
 1801 CAGCATGAGCACATTTCTCAAGTTTCTATGGAGTGTGGGGGATGGGGACCCCTCATCATGGTCTTTGAATACATGAAGCATGGAGACCTGAATAGTTTCTCAGGGGCCCATGGGCCAGAT
 565 Q H E H I V K F Y G V C G D G D P L I M V F E Y M K H G D L N K F L R A H G P D
 1921 GCAATGATCTGTGATGACAGCCAGCCAGGCGAGGTGAGCTGGGCTCTCCCAAATGCTCCACATTCGCCAGTCAGATCGCCTCGGTATGGTGTACCTGGGCTCCAGCCTTT
 605 A M I L V D G Q P R Q A K G E L G L S Q M L H I A S Q I A S G M V Y L A S Q H F
 2041 GTGCACCGAGACCTGGCCACAGGAACCTGCTGTGGAGCGAATCTGCTAGTGAAGATTGGGGACTTCGGCATGTCCAGAGATGCTCTACAGCAGGATTATTACAGGCTCTTTAATCCA
 645 V H R D L A T R N C L V G A N L L V K I G D F G M S R D V Y S T D Y Y R L F N P
 2161 TCTGGAATGATTTTGTATATGCTGTGAGTGGGAGACACACCATGCTCCCAATTCGCTGGATGCTCTGAAAGCATCATGTACCGGAAGTTCACTACAGAGAGTGTATGGAGC
 685 S G N D F C I W C E V G G H T M L P I R W M P P E S I M Y R K F T T E S D V W S
 2281 TTCGGGGTGATCTCTGGGAGATCTTCACCTATGGAAGCAGCGCATGGTTCCAACTCTCAAACACCGAGGTCTATGAGTGCAATTACCCAAAGGTCTGTGTTTTCGAGCGGCCCGAGCTGCG
 725 F G V I L W E I F T Y G K Q P W F Q L S N T E V I E C I T Q G R V L E R P R V C
 2401 OCCAAGAGGTGTACGATGTATGCTGGGTGCTGGCAGAGGGAAACACAGCAGCGGTGTGAACATCAAGGAGATCTACAAATCTCTCCATGCTTTGGGGAAGGCCACCCCAATCTACCTG
 765 P K E V Y D V M L G C W Q R E P Q Q R L N I K E I Y K I L H A L G K A T P I Y L
 2521 GACATTTCTGGCTAGTGGTGGTGTGATGAAATTCATCTCTGCTGCTGCTCCTCTCCACCTCACAACCTCCTTCCATCTCTTGGACTGAGGCGAATC
 805 D I L G O
 2641 TTCATATAAACTCAAGTGCCTGCTACACATACACACTGAAGAAAGGAAAAAGAAAAAGAAAAAGAAAAAGCGG

FIG. 2B

1600 TGGTCTTTTCAACATAGACAATCATGGGATATTAACTTGAAGGACAAATAGAGATCATCTAGTCCCATCAACTCACTATATATATATGAGGAACCTGAGGTCCAGAGTGGGAACTGTCT
498 W V F S N I D N H G I L N L K D N R D H L V P S T H Y I Y E E P E V Q S G E V S
1720 TACCCAGGTCAATGGTTTCAGAGAAATTATGTTGAAATCCAAATAGCCTTCCGGGACATTCGCAATGGCATCTATGTTGAGGATGTCAAATGTTTATTTTCAGCMAAGGA
538 Y P R S H G F R E I M L N P I S L P G H S K P L N H G I Y V E D V N V Y F S K G
1840 CGTCATGGCTTTTAAAAAC
578 R H G F O

FIG. 2C

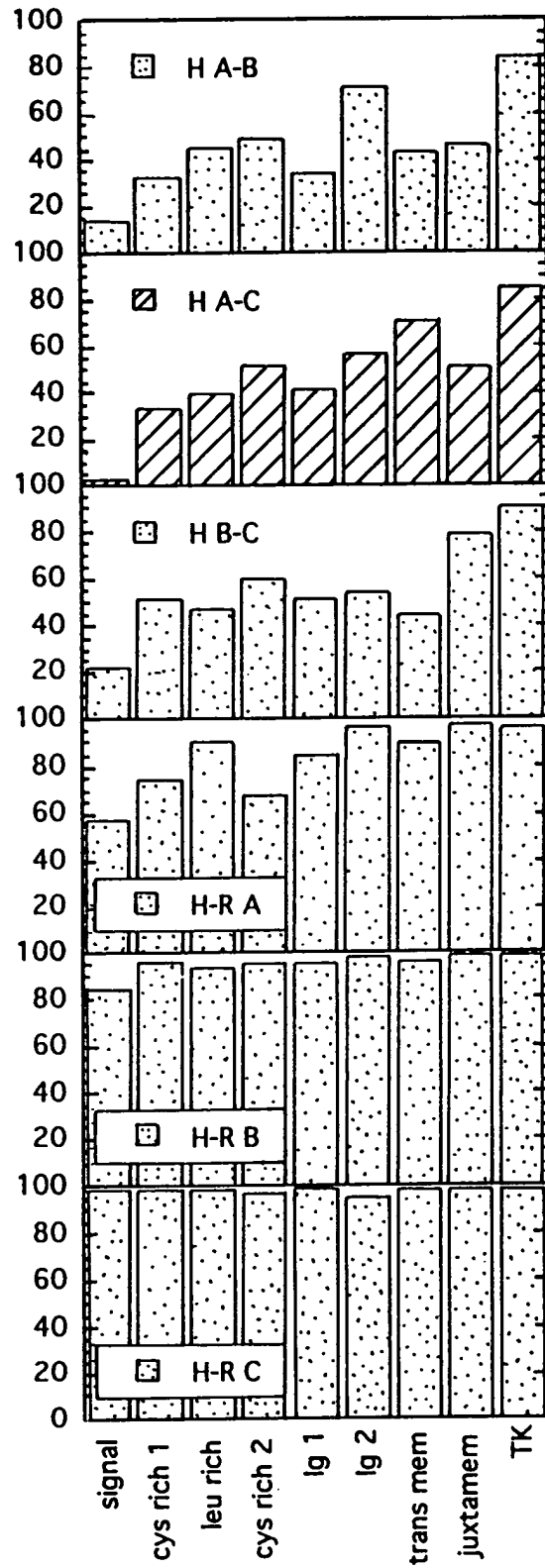


FIG. 3

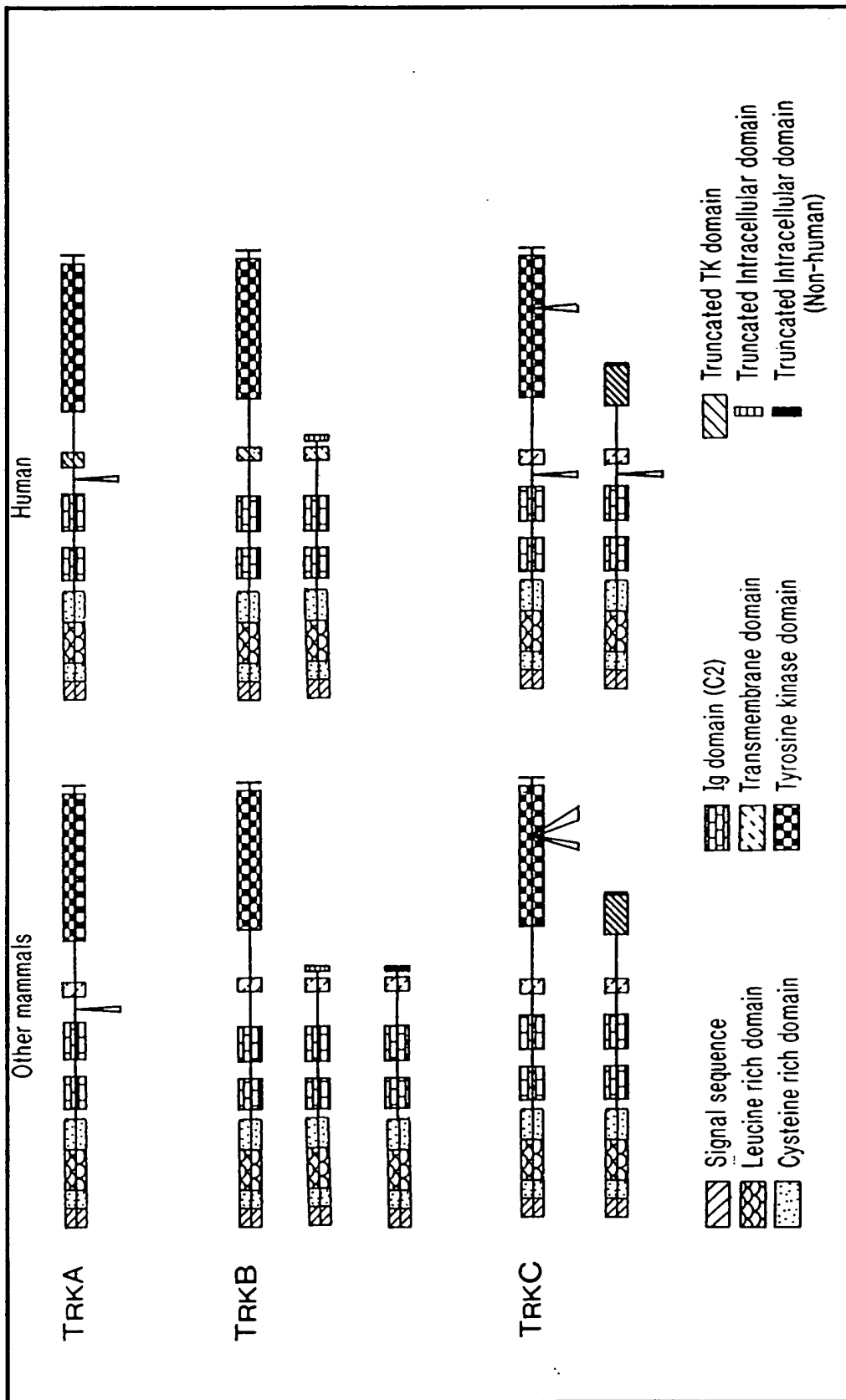


FIG. 4

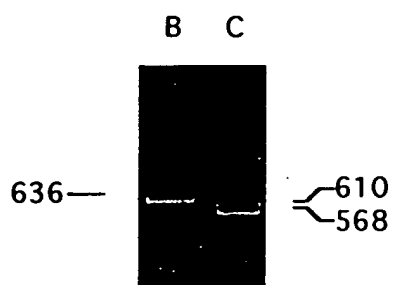


FIG. 5

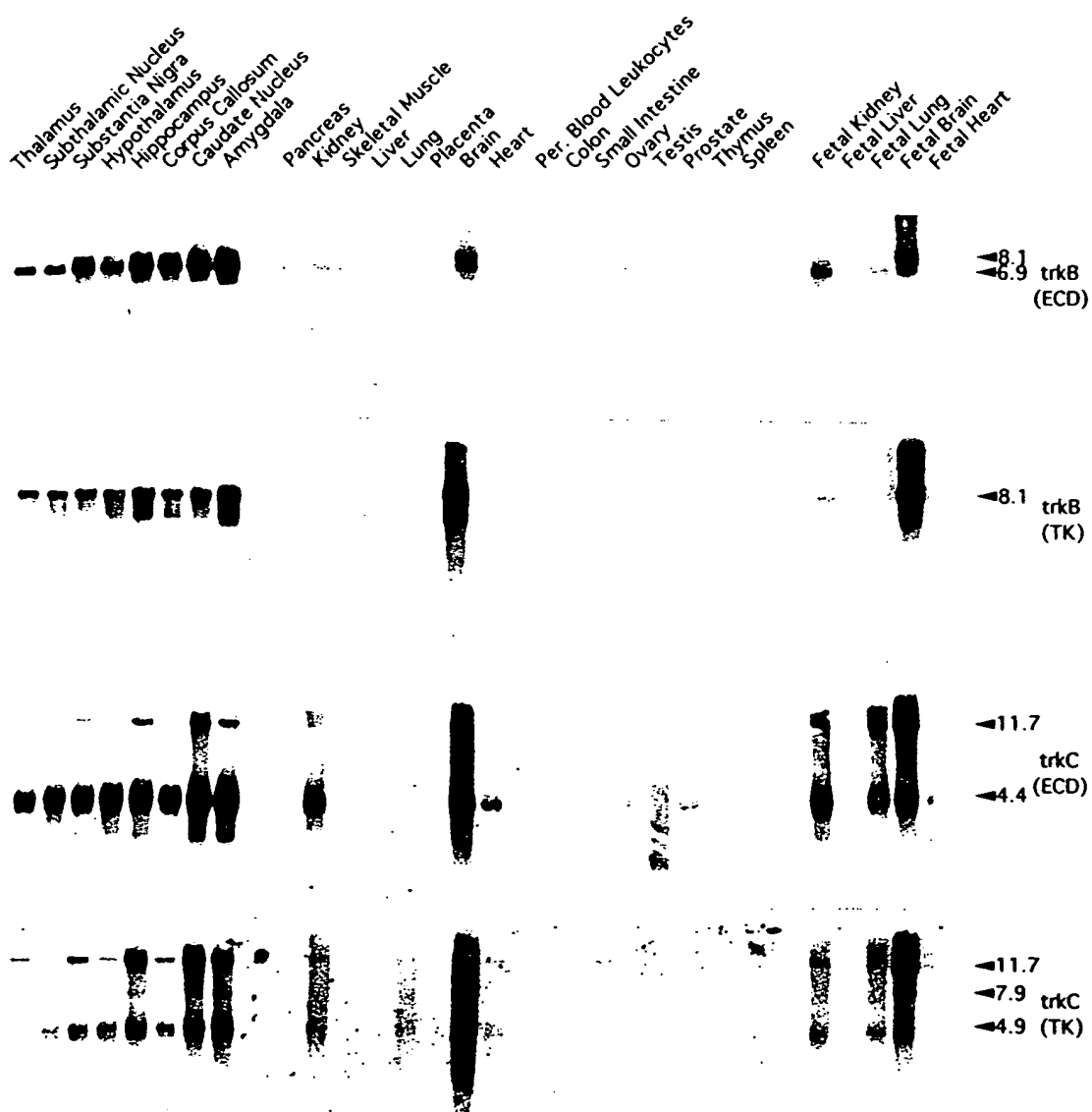


FIG. 6



FIG. 7A



FIG. 7B



FIG. 7C

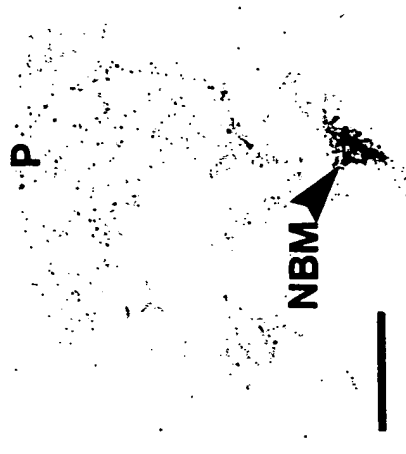


FIG. 7D

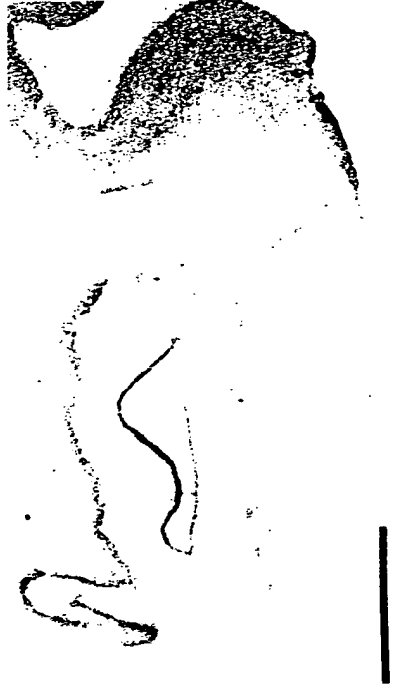


FIG. 7E

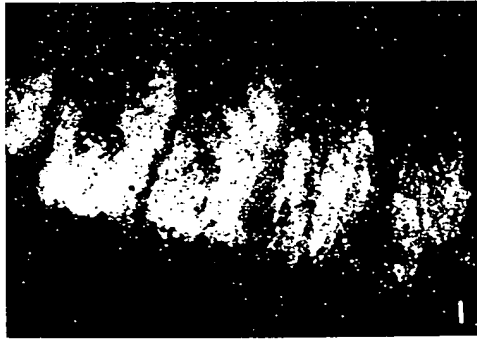


FIG. 8A

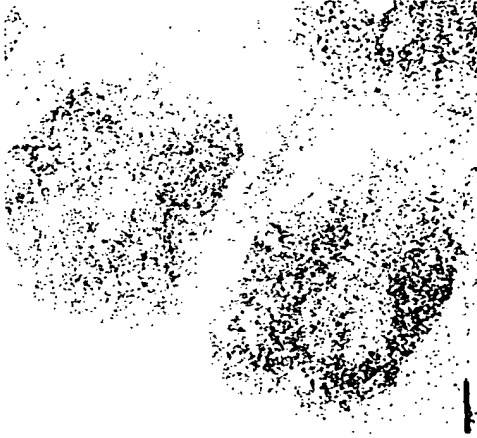


FIG. 8B

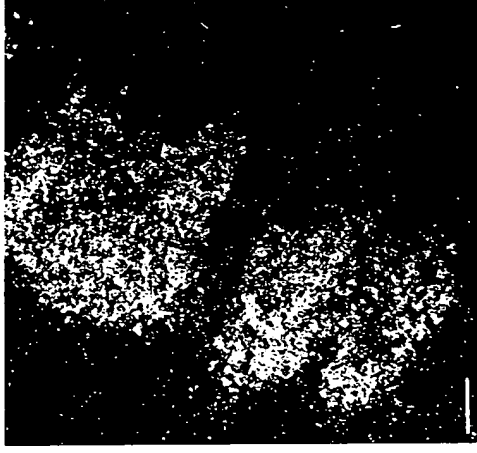


FIG. 8C

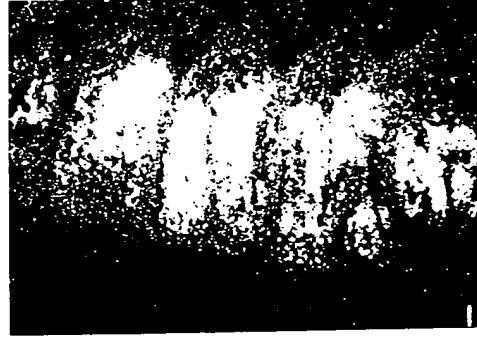


FIG. 8D

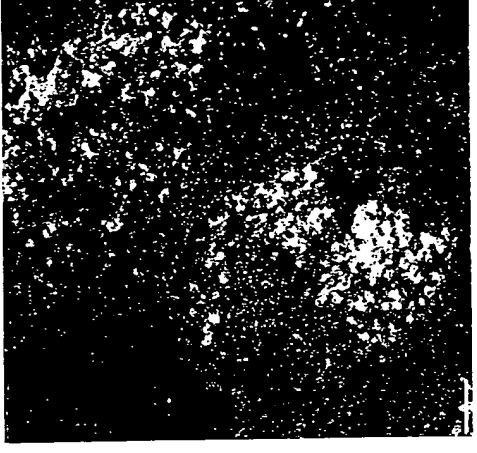


FIG. 8E

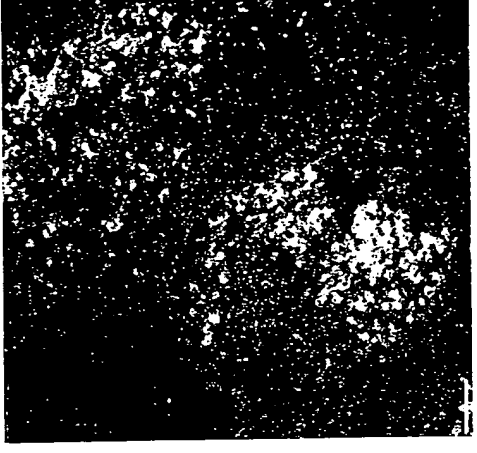


FIG. 8F

09966147 .092701

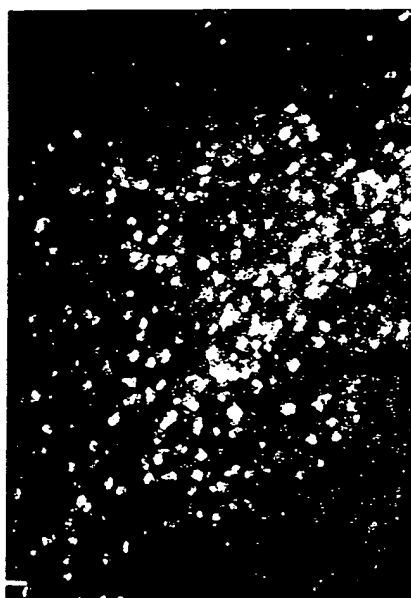


FIG. 9A

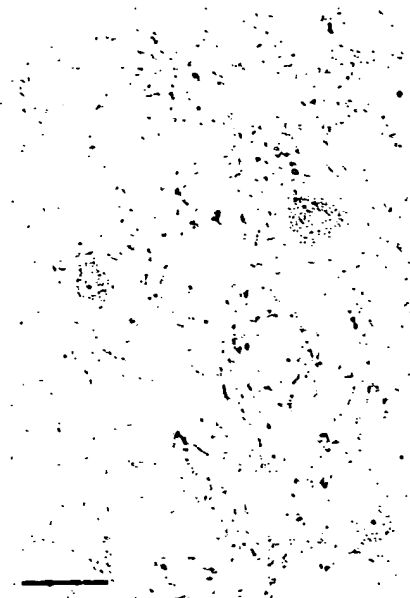


FIG. 9B

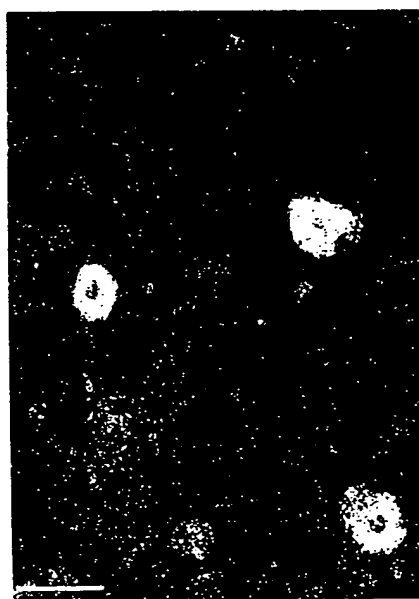


FIG. 9C



FIG. 9D

09966147-092701

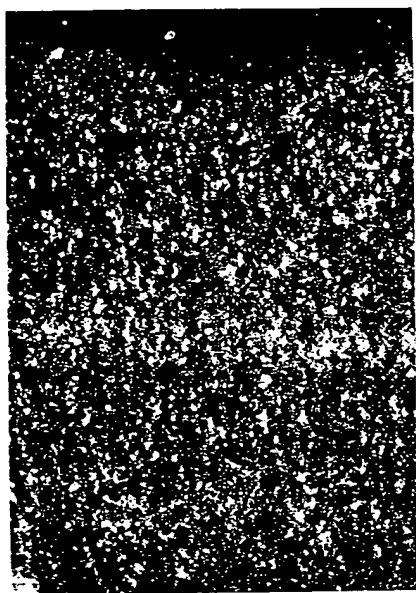


FIG. 9E



FIG. 9F

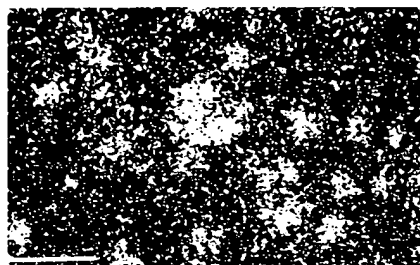
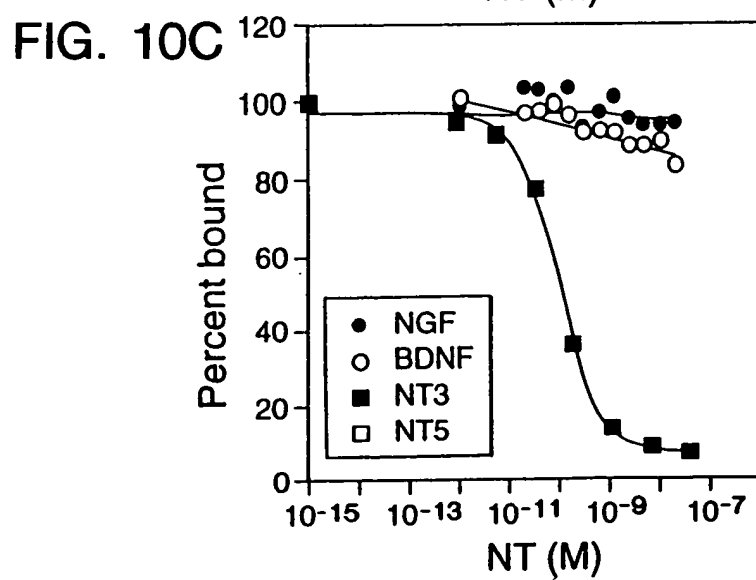
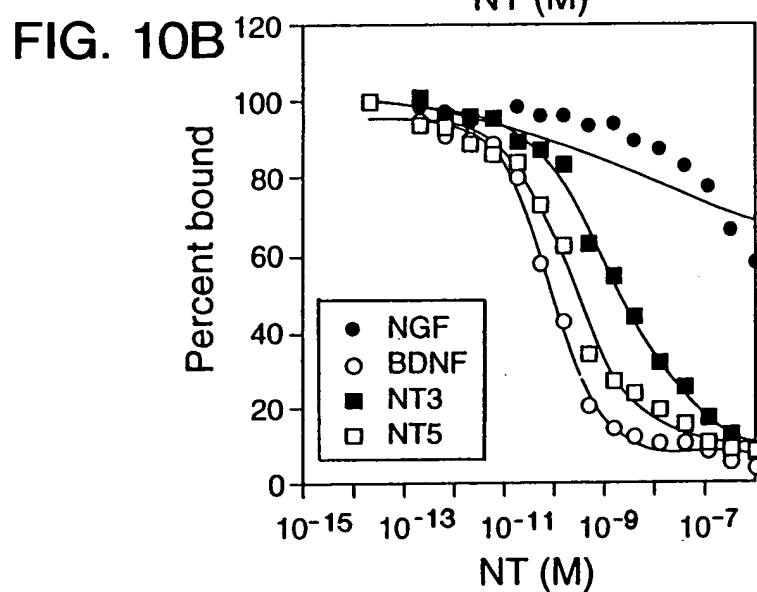
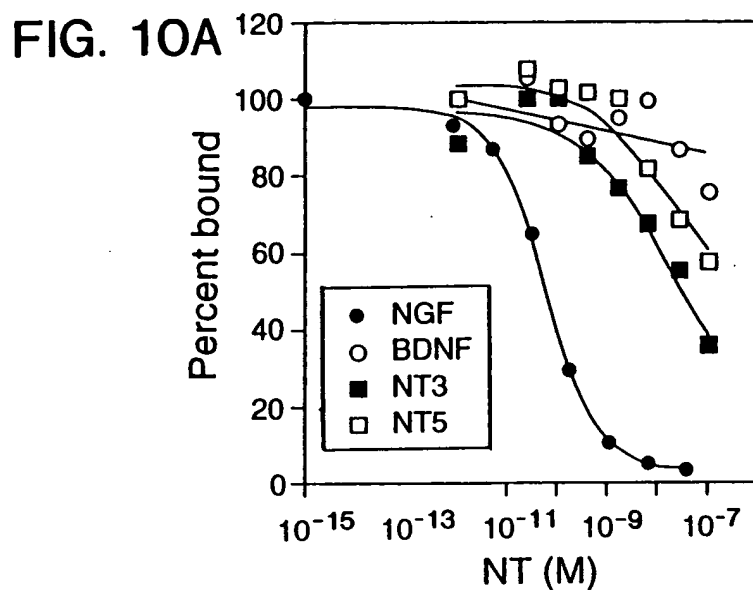


FIG. 9G



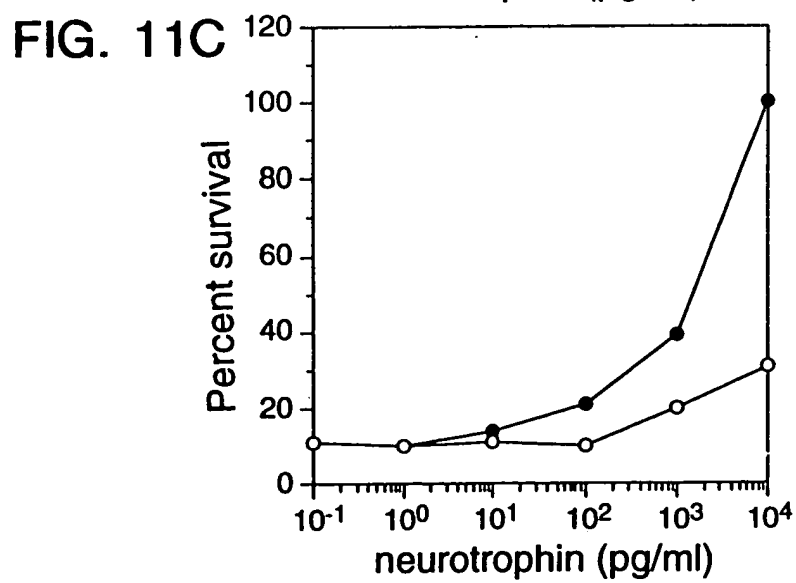
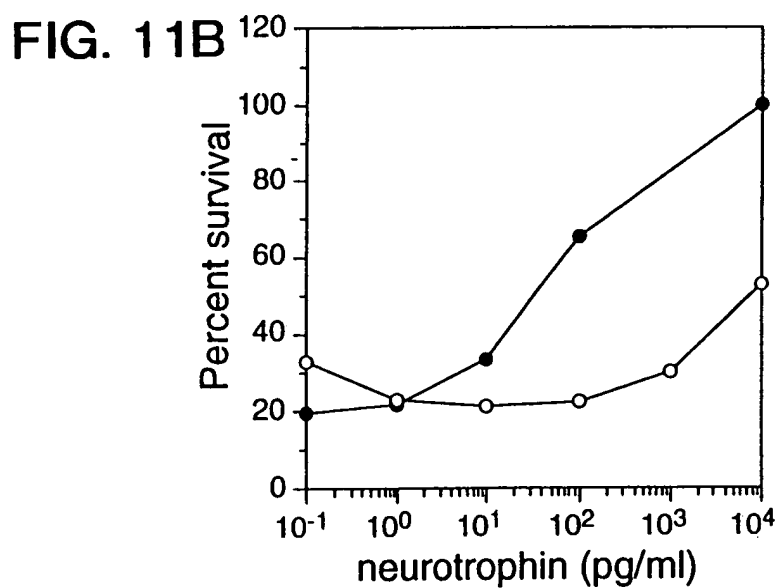
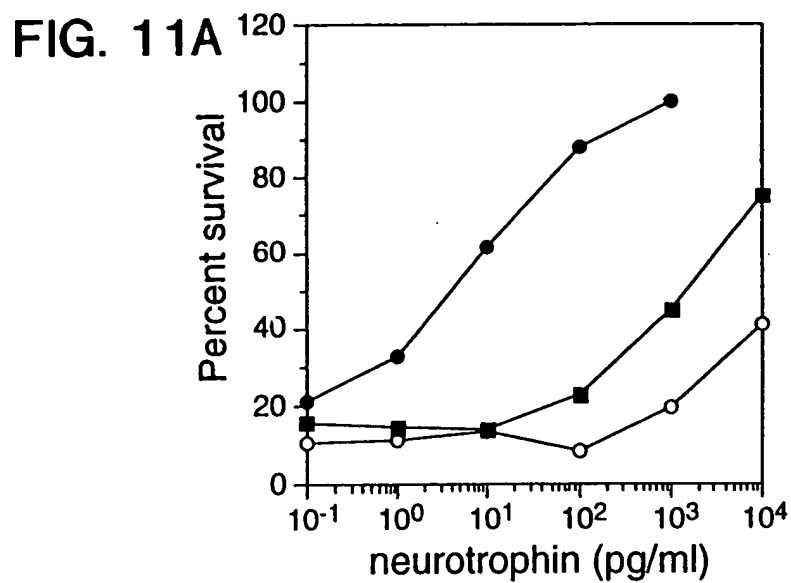
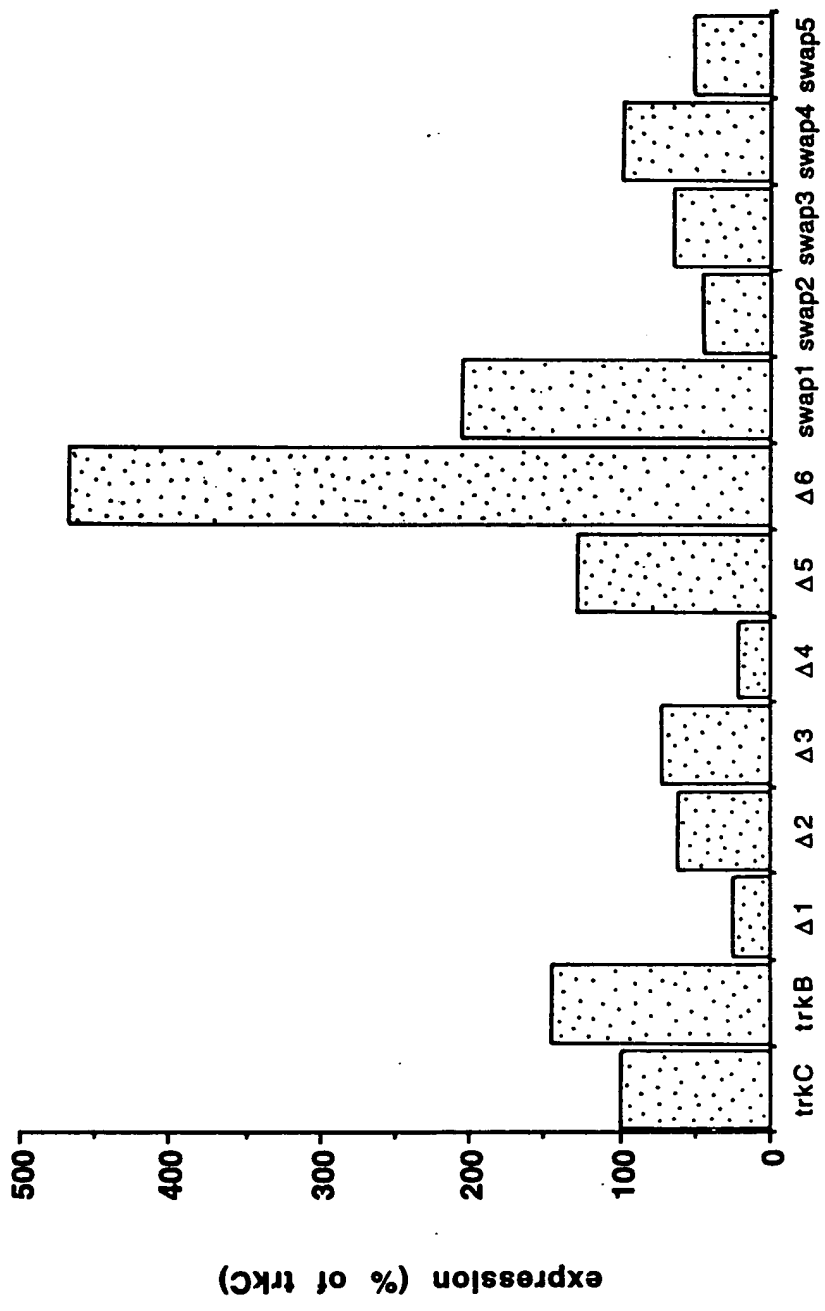




FIG. 12



receptor variant

FIG. 13

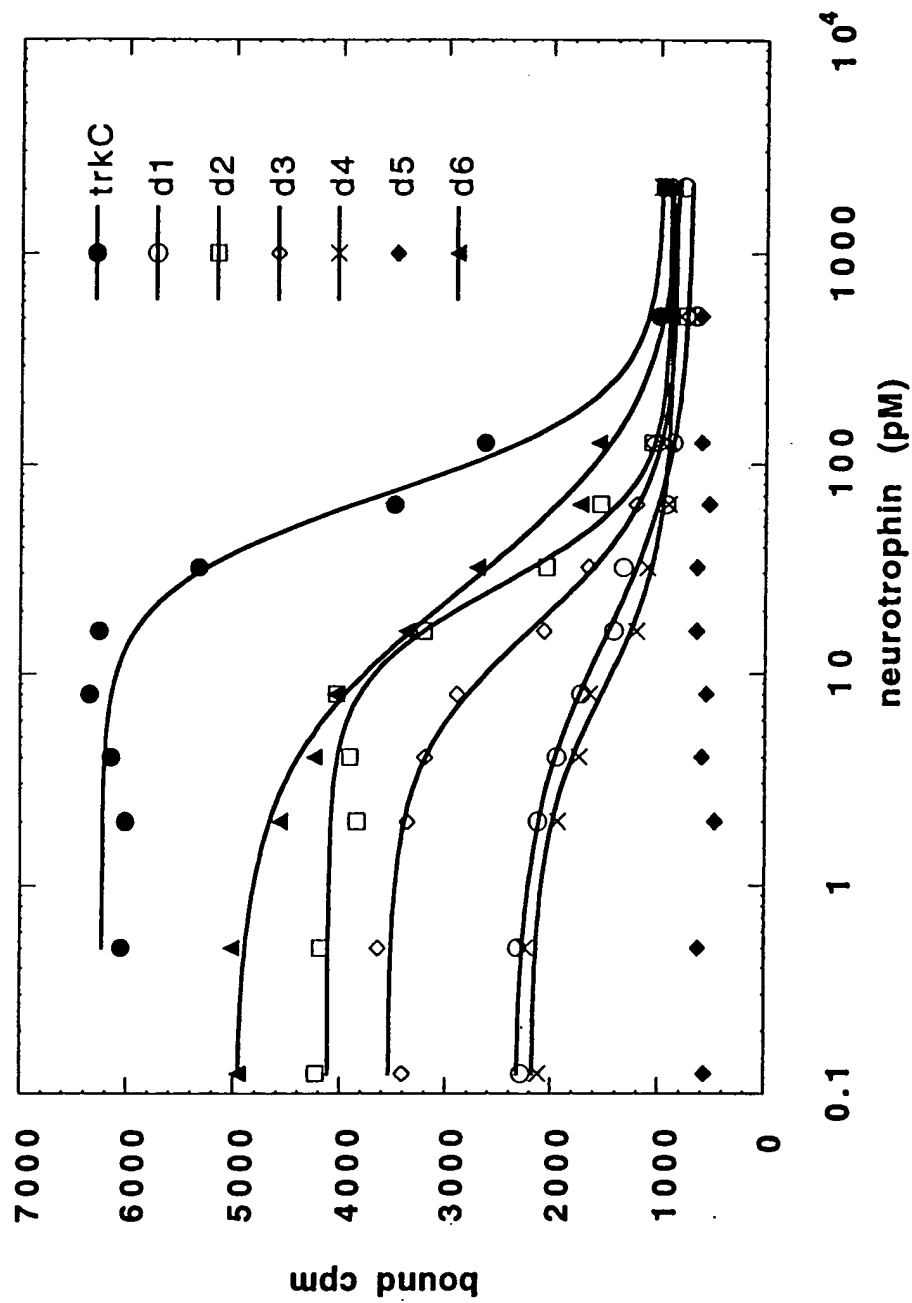


FIG. 14A

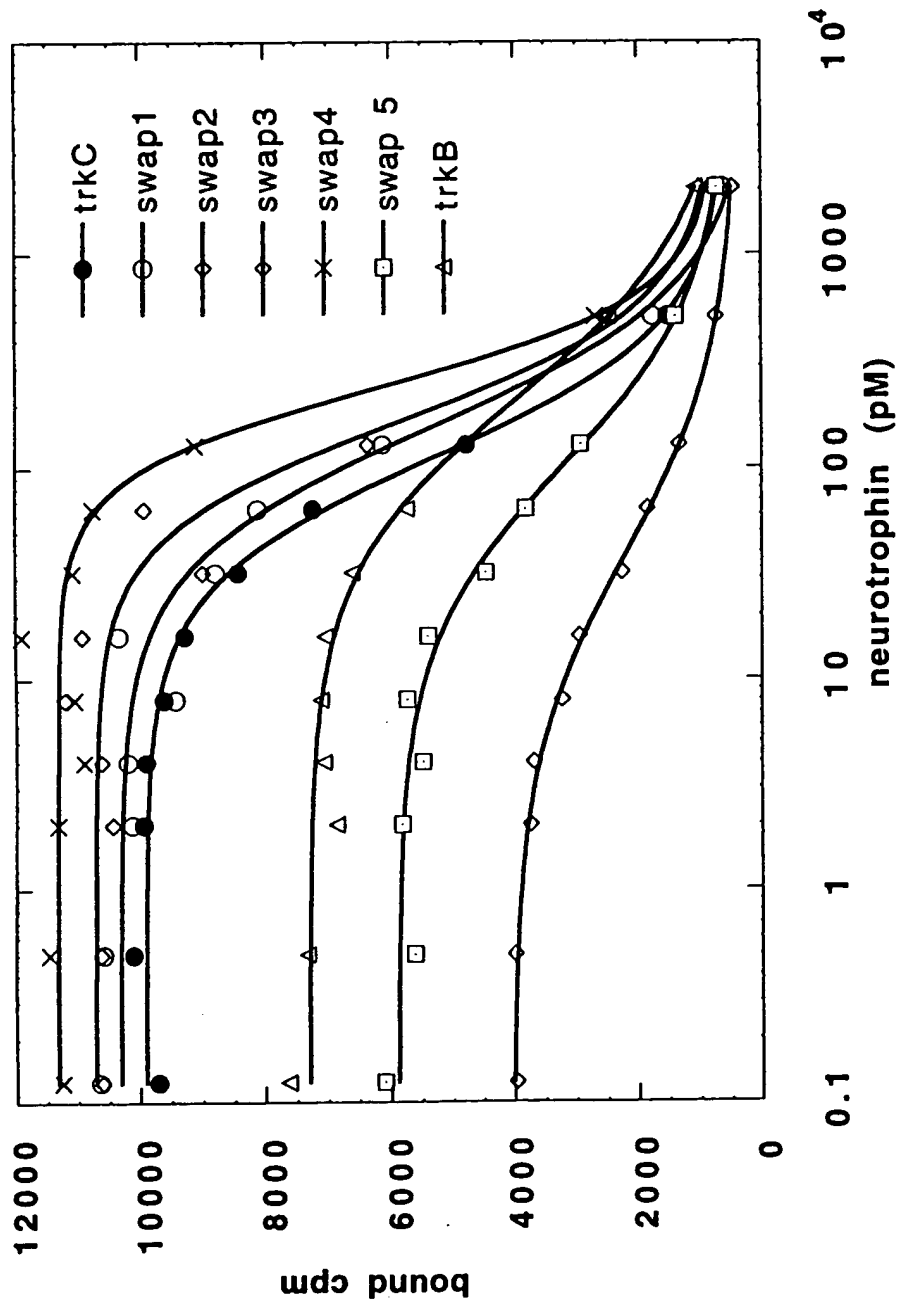


FIG. 14B

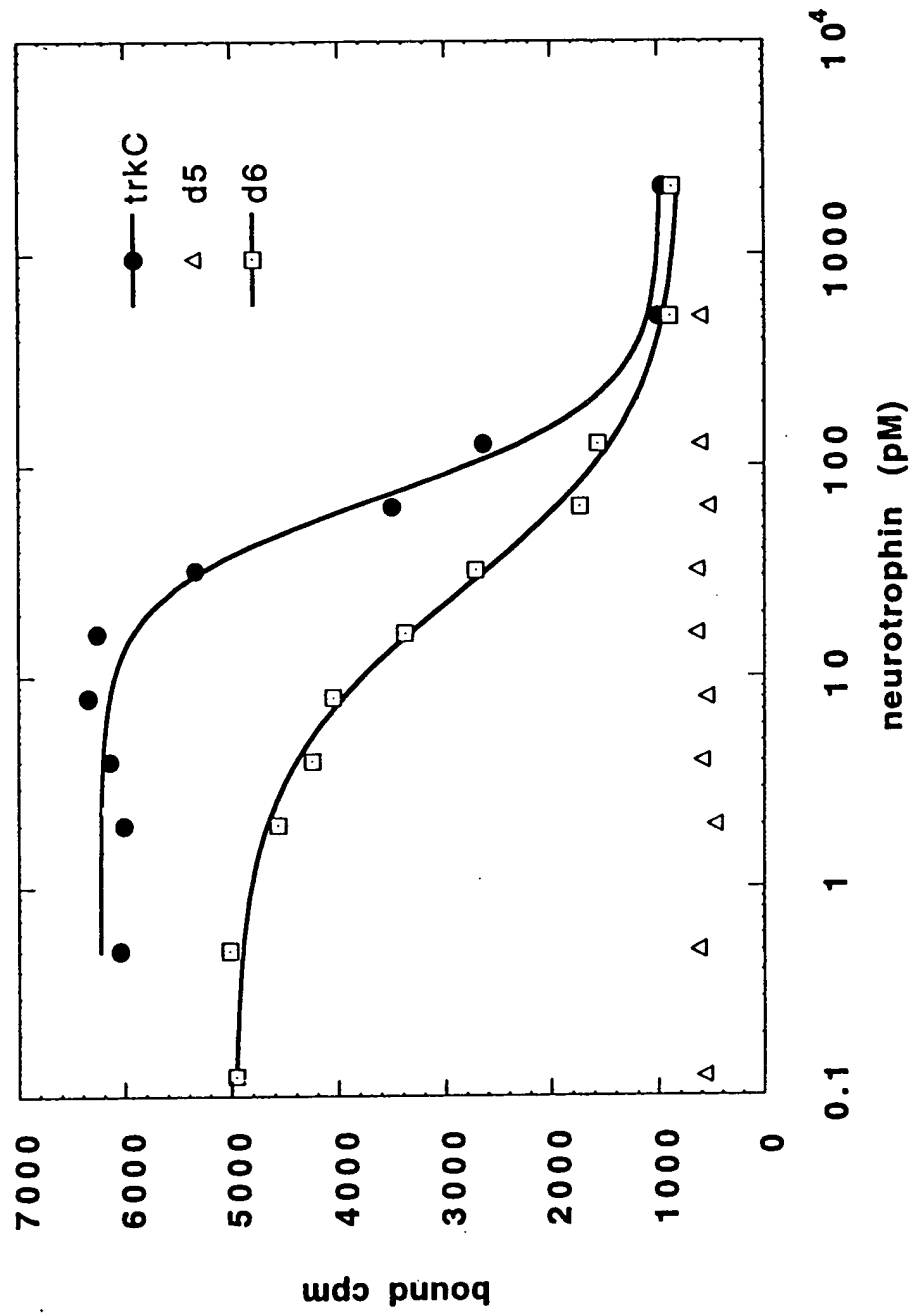


FIG. 14C

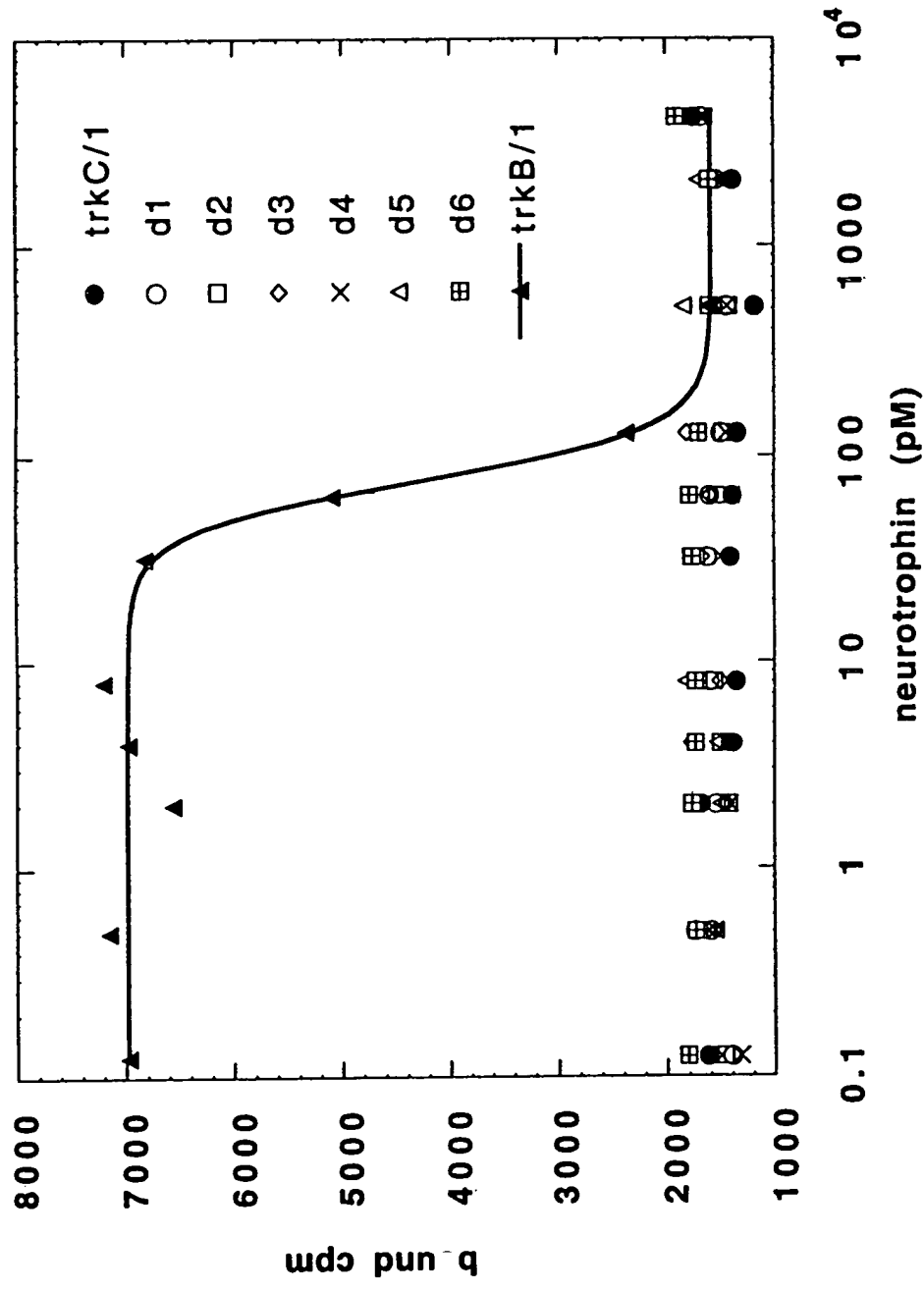


FIG. 15A

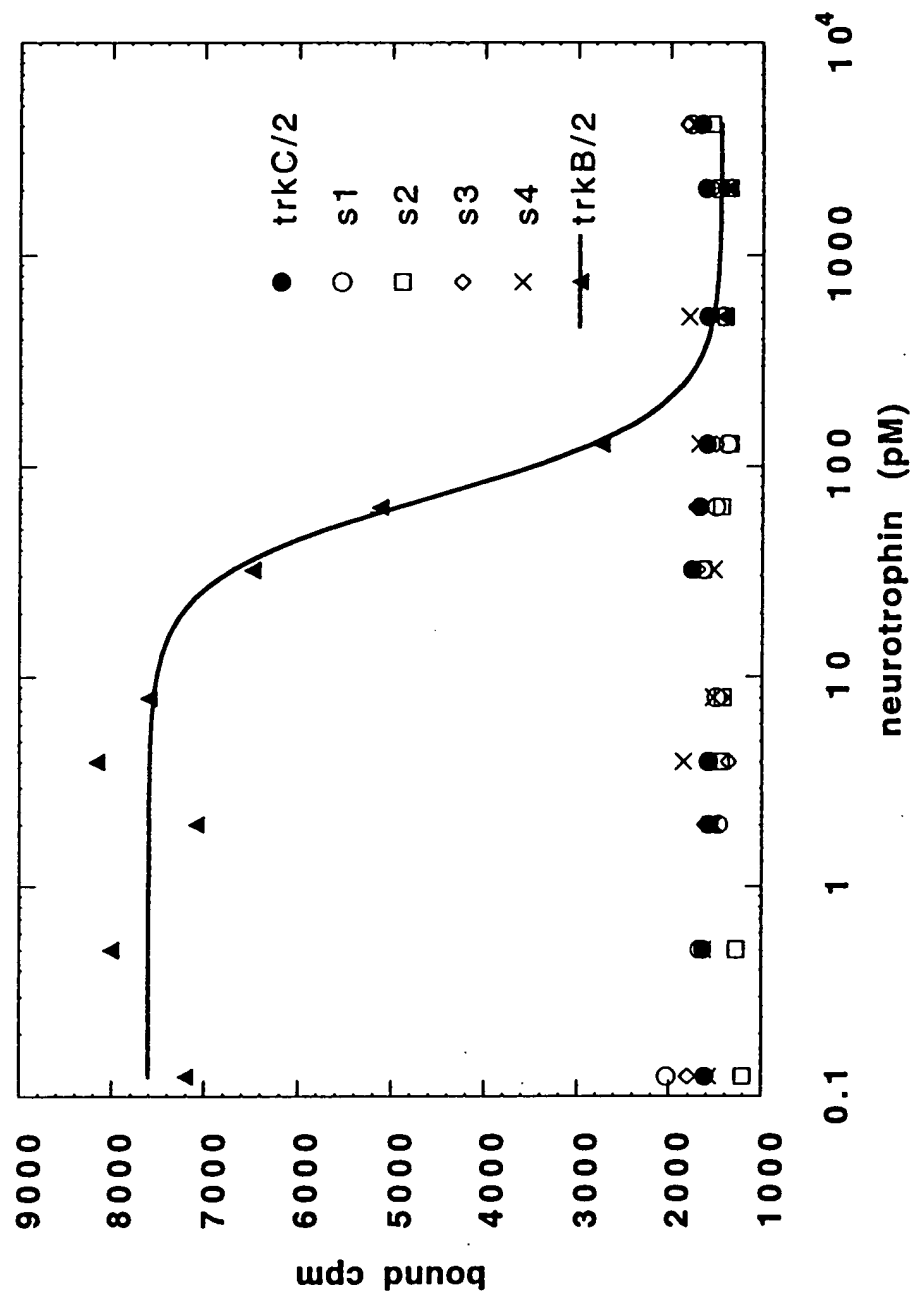


FIG. 15B

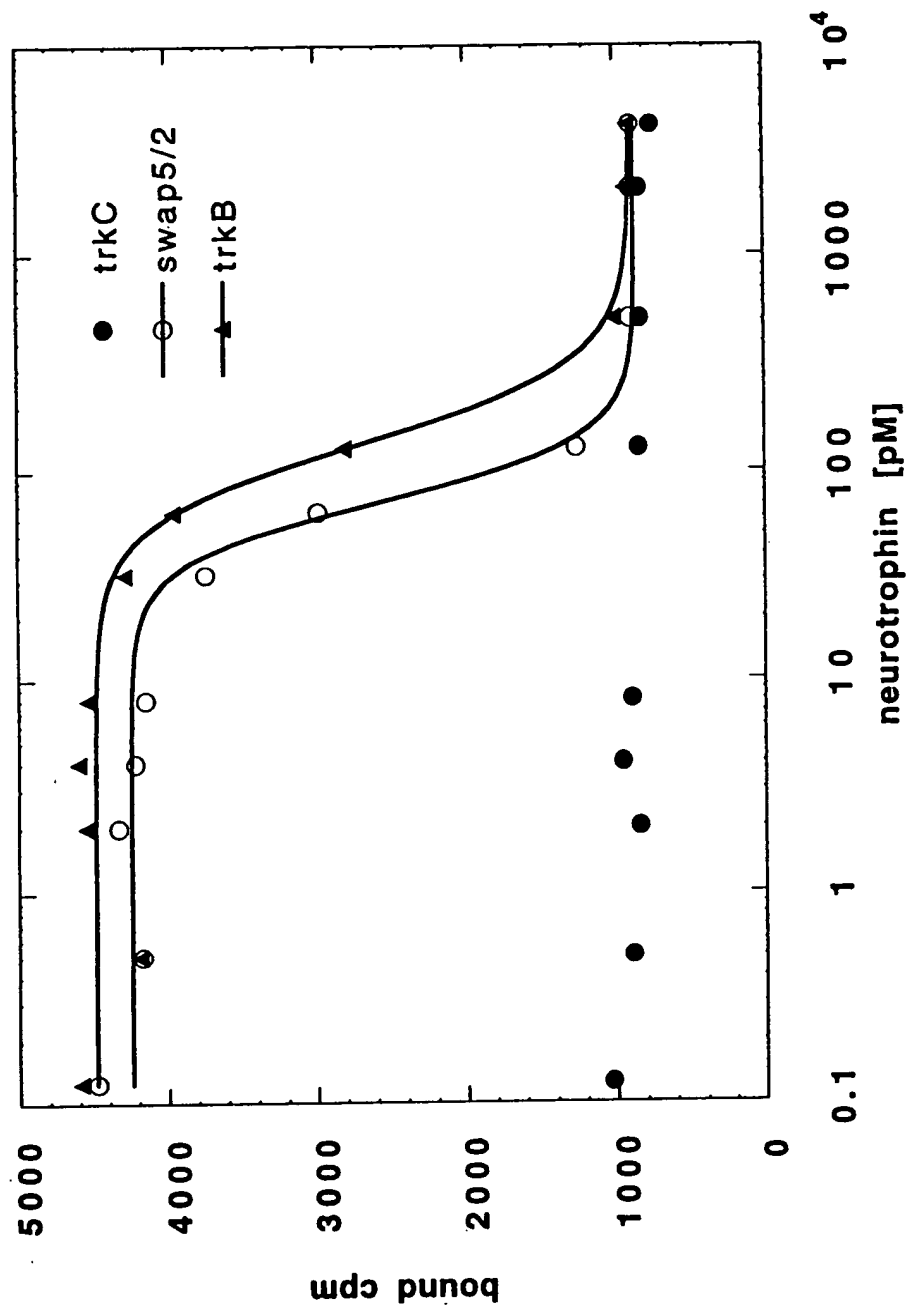


FIG. 15C

		Signal	
trkA	1	HLRGRRGOLGWHSWAAGPGLLAWLILAS - - - - AGAAPCPDACCP	
trkB	1	- - - - MSSWIRWHGPAMARLWGFCWLVGFW - - - - RAAFAACPTS - CK	
trkC	1	- - - - MDVSL - - - CPAKCSFWRI - FLGSVWLDYVGSVLACPAN - CV	
		Cysteine Rich I	
		HGSSGLRCTR - DGALDSLHHLPG - - - - - AENLTIELYIENQQ	
		CSASRIWCSDPSPGIVAFPRLEPNVSD - - - - - PENITTEIFIANOK	
		CSKTEINCRRPDDGNL - FPLLEGODSGNSNGNANINITDISRNITSIHIENWR	
		Leucine Rich	
trkA	78	HLOHLELRDLRGLGELRNLTIVKSGLRFVAPDAFHFTPRLSRLNLSF	
trkB	78	RLEIINEDDVEAYVGLRNLTIVDSGLKFVAHKAFLKNSNLQHINFTIR	
trkC	90	SLHTLNAYDMELYTGLOKLTIKNSGLRSIQPRAFAKNPHLRYINLSS	
		Cysteine Rich II	
		HALESLSWKTVOGLSLQELVLSGNPLHCSICALRWLORWEEEGLGGVPEQKLQC	
		NKLTSLSRKHFRLDLSELILVGNPFTCSCDIMWIKTLOE - AKSSPDITQDLYC	
		NRLTTLWOLFOTLSLRELOLEQNFNCSCDIRWMOLWEOEGEAKLNSQNLVC	
trkA	178	HGQG - - - PLAHMPNASCQVPTLKVOVPNASVDYGGDDVLLRCQVEGR	
trkB	177	LNESKNIPPLANLOIPNCGLPNSANLAAPNLTVEEGKSIITLSCSVAGD	
trkC	180	INADGSOLPLFRMNI SOC DLPEISVSHVNLTVREGDNNAVITCNGSGS	
		Immunoglobulin I	
		GLEQAGWILTELEQSAIVMK - - - GGLPSLGLTLANVTSDLNRKNLTCWAEND	
		PVPNMYWDVGNLVSKHMHNET - - - SHTQG - SLRITNISSDDSGKQISCVAENL	
		PLPDVDWIVITGLOSINTHOTNLNWTNVHAINLTLVNVTSEDNMGFTLTICIAENV	

FIG. 16A

<i>trkA</i>	271	VGRAEVSVQVNVSFPA	SVQ - LHTAVEMHHWC	IPFSVDGOPAPSLRWL
<i>trkB</i>	272	VGEDODSVNLT	VHFAPTITFL	ESPTSDHHWCIPFTVKG
<i>trkC</i>	290	VGMSNASVAL	TVYYP	PRVVSLEELRLEHCIEFVVRGNPPPTLHWL
		<u>Immunoglobulin II</u>		
		FNGSVLNETS	FI	FTFLEPAANETVRHGCLRLNQPT
		YNGAILNESK	YICTKI	H - VTNHTEYHGCLQLDNPT
		HNGOPLRESK	IIHVEYY -	OEGEIS - EGCLLFNKP
		THYNNGN	YTLIAKN	PLGT
<i>trkA</i>	370	ASASIMAAFM	- - - - -	DNPF - - - - - EF - NPEDPI
<i>trkB</i>	370	DEKOISAHFM	GWPGIDDG	ANPNYPDVIYEDYGTA
<i>trkC</i>	387	ANQTINGHFL	- - - - -	KEPFEST - DMF - ILFDEV
		<u>Transmembrane</u>		
		- TSGDP	VEKKDET - - -	PFGVSAVGLAVFACLF
		IPSTD	VTDK	TGREHLSVYAVVVIASVVG
		- PPIT	VTHKPEED - - -	TFGVSI
		AVGLAA	AFACVLLV	LVLFV
		<u>Juxtamembrane</u>		
<i>trkA</i>	448	RP - AVL	APEDGLAMSLH	FM
<i>trkB</i>	468	GPA	SVISNDDDSAS	PLHHISNGSNT
<i>trkC</i>	468	GPVAV	ISGEE	DSASPLHHINHG
		ITTP	SSLDAG	PD
		TVV	IGMT	RIPI
		VE		
		<u>Transmembrane</u>		
		NPOYF	- - - - -	SDACVHHIKRR
		DI	VSKWEL	GEGAFGKV
		FLA	ECHN	LLPEOD
		NPOYF	GITNSOLK	PPDTFVQH
		IKRR	HNIVL	KREL
		GEGAFGKV	FLAECYN	LCPEOD
		NPOYF	ROGHNCH	KPPDTYVQH
		IKRR	DI	VSKWEL
		GEGAFGKV	FLAECYN	LSPTKD

FIG. 16B

532	trkA	KMLVAVKALKEASESARODFOREAEELLTMLQHQHIVRFFGVCVTEGRP
566	trkB	KILVAVKTLKDAASDNARKDFHREAEELLTNLQHEHIVKFGVCVEGDP
566	trkC	KMLVAVKALKDPTLAARKDFOREAEELLTNLQHEHIVKFGVCGDGP
Tyrosine Kinase		
		LLMVFEYMRHGDNLNRFLRSHGPDAKLLAGGEDV-APGPLGLGQLLAVASQVAA
		LIMVFEYMKKHGDLNKFLLRAHGPDADVLMAEGNPP--TELTSOMLHIAQQIAA
		LIMVFEYMKKHGDLNKFLLRAHGPDAMILVDGOPROAKGELGLSOMLHIASOIAS
<hr/>		
631	trkA	GMVYLAGLHFVHRDLATRNCCLVGGGLVVKIGDFGMSRDIYSTDYR-
663	trkB	GMVYLASQHFVHRDLATRNCCLVGENLLVKIGDFGMSRDVYSTDYR-
666	trkC	GMVYLASQHFVHRDLATRNCCLVGANLLVKIGDFGMSRDVYSTDYRL
<hr/>		
		- - - - - VGGRTMLPIRWMPPEESILYRKFTTESDVWSFGVVLWEIFT
		- - - - - VGGHTMLPIRWMPPEESIMYRKFTTESDVWSLGVVLWEIFT
		FNPSGNDFCIWCEVGGHTMLPIRWMPPEESIMYRKFTTESDVWSFGVILWEIFT
<hr/>		
717	trkA	YGKOPWYQLSNTEAIDCITOGRELERPRACPPPEVYAIMRGCWOREPO
749	trkB	YGKOPWYQLSNNEVIECITOGRVLORPRTCPOEVYELMLGCMWOREPH
766	trkC	YGKOPWFOLSNTEVIECITOGRVLERPRVCPKEVYDVMLGCMWOREPO
<hr/>		
		QRHSIKDVHARLQALAOAPPVYLDVLG
		MRKNIKGIHTLLQNLAKASPVYLDILG
		ORLNIXEIYKILHALGKATPIYLDILG

FIG. 16C

1042260 44799660

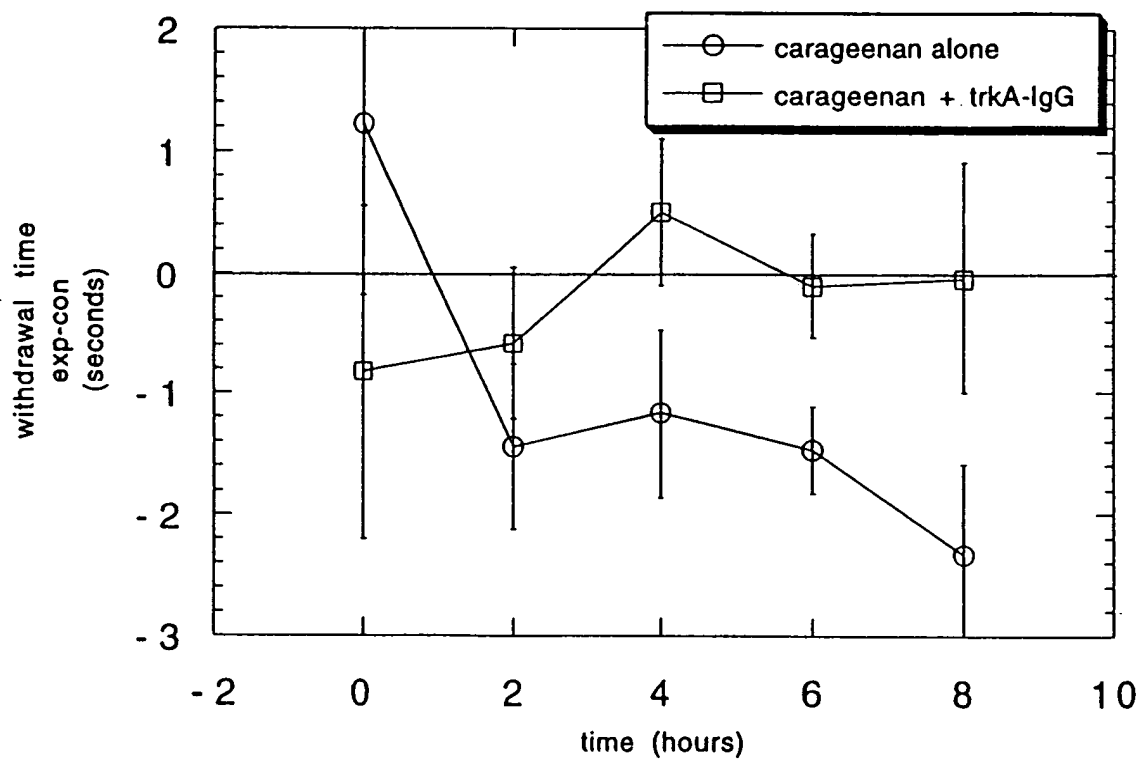


FIG. 17

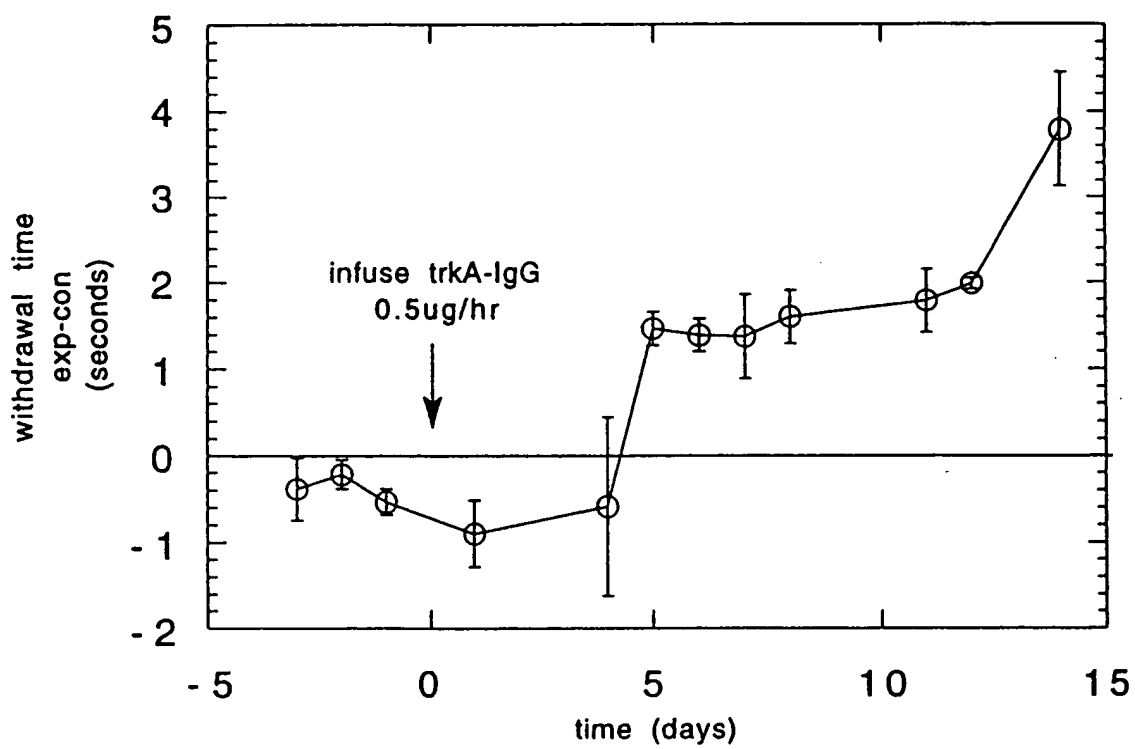


FIG. 18